

SEQUENCE LISTING

SEQ. ID No. 1

LENGTH: 271

TYPE: amino acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro  
1 5 10 15  
Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr  
20 25 30  
Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met  
35 40 45  
Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser  
50 55 60  
Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu  
65 70 75  
Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr  
20 80 85 90  
Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala  
95 100 105  
Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr  
110 115 120

Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr  
125 130 135  
Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile  
140 145 150  
5 Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr  
155 160 165  
Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser  
170 175 180  
Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr  
10 185 190 195  
Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile  
200 205 210  
Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg  
215 220 225  
15 Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile  
230 235 240  
Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala  
245 250 255  
Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys  
20 260 265 270  
Thr

SEQ. ID No. 2

LENGTH: 25

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Asp Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His  
1 5 10 15  
Gly Pro Glu Ile Leu Asp Val Pro Ser Thr  
20 25

SEQ. ID No. 3

10 LENGTH: 155

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

15 SEQUENCE:

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp  
1 5 10 15  
Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys  
20 25 30  
20 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro  
35 40 45  
Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile  
50 55 60  
Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys

65                    70                    75  
Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg  
80                    85                    90  
Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu  
5                    95                    100                    105  
Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr  
110                    115                    120  
Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu  
125                    130                    135  
10 Gly Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro  
140                    145                    150  
Met Ser Ala Lys Ser  
155

SEQ. ID No. 4

15 LENGTH: 432

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

20 SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1                    5                    10                    15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20                    25                    30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
5 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Val Tyr Glu Gln  
65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
10 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
95 100 105  
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
110 115 120  
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
125 130 135  
15 Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
140 145 150  
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg  
155 160 165  
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
20 170 175 180  
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
185 190 195  
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
200 205 210  
25 Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe

	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
5	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ala Gly Ser Ile Thr Thr		
	275	280	285
10	Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro		
	290	295	300
	Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly		
	305	310	315
	Phe Phe Leu Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg		
15	320	325	330
	Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu		
	335	340	345
	Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu		
	350	355	360
20	Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr		
	365	370	375
	Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn		
	380	385	390
	Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys		
25	395	400	405

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln  
410 415 420  
Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
425 430

5 SEQ. ID NO. 5

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
15 20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
5	125	130	135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
10	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
15	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
20	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ala Gly Ser Ile Thr Thr		
25	275	280	285

Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro  
290 295 300  
Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly  
305 310 315  
5 Phe Phe Leu Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg  
320 325 330  
Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu  
335 340 345  
Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu  
10 350 355 360  
Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr  
365 370 375  
Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn  
380 385 390  
15 Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys  
395 400 405  
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln  
410 415 420  
Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Ala Ser Asp Glu Leu  
20 425 430 435  
Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu  
440 445 450  
Ile Leu Asp Val Pro Ser Thr  
455

SEQ. ID No. 6

LENGTH: 186

TYPE: amino acid

STRANDEDNESS: single

5

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Ile Arg Gly Leu Lys Gly Thr Lys Gly Glu Lys Gly Glu Asp  
1 5 10 15  
Gly Phe Pro Gly Phe Lys Gly Asp Met Gly Ile Lys Gly Asp Arg  
10 20 25 30  
Gly Glu Ile Gly Pro Pro Gly Pro Arg Gly Glu Asp Gly Pro Glu  
35 40 45  
Gly Pro Lys Gly Arg Gly Pro Asn Gly Asp Pro Gly Pro Leu  
50 55 60  
Gly Pro Pro Gly Glu Lys Gly Lys Leu Gly Val Pro Gly Leu Pro  
65 70 75  
Gly Tyr Pro Gly Arg Gln Gly Pro Lys Gly Ser Ile Gly Phe Pro  
80 85 90  
20 Gly Phe Pro Gly Ala Asn Gly Glu Lys Gly Gly Arg Gly Thr Pro  
95 100 105  
Gly Lys Pro Gly Pro Arg Gly Gln Arg Gly Pro Thr Gly Pro Arg  
110 115 120  
Gly Glu Arg Gly Pro Arg Gly Ile Thr Gly Lys Pro Gly Pro Lys  
25 125 130 135

Gly Asn Ser Gly Gly Asp Gly Pro Ala Gly Pro Pro Gly Glu Arg  
140 145 150  
Gly Pro Asn Gly Pro Gln Gly Pro Thr Gly Phe Pro Gly Pro Lys  
155 160 165  
5 Gly Pro Pro Gly Pro Pro Gly Lys Asp Gly Leu Pro Gly His Pro  
170 175 180  
Gly Gln Arg Gly Glu Thr  
185

SEQ. ID No. 7

LENGTH: 464

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
20 Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

	65	70	75
	His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp		
	80	85	90
	Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe		
5	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
	125	130	135
10	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
15	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
	200	205	210
20	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
25	245	250	255

Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
260 265 270  
Thr Glu Ile Asp Lys Pro Ser Met Gly Ile Arg Gly Leu Lys Gly  
275 280 285  
5 Thr Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro Gly Phe Lys Gly  
290 295 300  
Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly Pro Pro Gly  
305 310 315  
Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg Gly Gly  
10 320 325 330  
Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys Gly  
335 340 345  
Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly  
350 355 360  
15 Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly  
365 370 375  
Glu Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly  
380 385 390  
Gln Arg Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly  
20 395 400 405  
Ile Thr Gly Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly  
410 415 420  
Pro Ala Gly Pro Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly  
425 430 435  
25 Pro Thr Gly Phe Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly

440

445

450

Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Glu Thr

455

460

SEQ. ID No. 8

5

LENGTH: 489

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

10

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

20 65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

95 100 105

Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
110 115 120  
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
125 130 135  
5 Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
140 145 150  
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg  
155 160 165  
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
170 175 180  
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
185 190 195  
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
200 205 210  
15 Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
215 220 225  
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys  
230 235 240  
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg  
20 245 250 255  
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
260 265 270  
Thr Glu Ile Asp Lys Pro Ser Met Gly Ile Arg Gly Leu Lys Gly  
275 280 285  
25 Thr Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro Gly Phe Lys Gly

290                    295                    300  
Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly Pro Pro Gly  
305                    310                    315  
Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg Gly Gly  
5                        320                    325                    330  
Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys Gly  
335                    340                    345  
Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly  
350                    355                    360  
Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly  
365                    370                    375  
Glu Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly  
380                    385                    390  
Gln Arg Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly  
395                    400                    405  
Ile Thr Gly Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly  
410                    415                    420  
Pro Ala Gly Pro Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly  
425                    430                    435  
20 Pro Thr Gly Phe Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly  
440                    445                    450  
Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Ala Ser Asp  
455                    460                    465  
Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly  
25                        470                    475                    480

Pro Glu Ile Leu Asp Val Pro Ser Thr

485

SEQ. ID No. 9

LENGTH: 36

5

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

10

AAACCATGGC AGTCAGCGAC GAGCTTCCCC AACTGG

36

SEQ. ID No. 10

LENGTH: 20

15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AATTGACAAA CCATCCATGG

20

SEQ. ID No. 11

20

LENGTH: 33

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCATTA~~AA~~AT CAGCTAGCAG CAGACATTGG AAG

33

5

SEQ. ID No. 12

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

TCTAGAGGAT CCTTAGCTAG CGCCTCTCTG TCCAGG

36

10  
9  
8  
7  
6  
5  
4  
3  
2  
1

SEQ. ID No. 13

LENGTH: 547

15

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20

Ala Ala Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln

5

10

15

Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val

20

25

30

Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr  
35 40 45  
Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val  
50 55 60  
5 Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val  
65 70 75  
Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val  
80 85 90  
Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val  
95 100 105  
10 Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys  
110 115 120  
Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn  
125 130 135  
15 Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser  
140 145 150  
Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr  
155 160 165  
Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile  
20 170 175 180  
Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu  
185 190 195  
Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg  
200 205 210  
25 Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser

215                    220                    225

Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu  
230                    235                    240

Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr  
5                        245                    250                    255

Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly  
260                    265                    270

Arg Lys Lys Thr Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe  
275                    280                    285

Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro  
290                    295                    300

Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu  
305                    310                    315

Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser  
320                    325                    330

Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val  
335                    340                    345

Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln  
350                    355                    360

20                        Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala  
365                    370                    375

Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg  
380                    385                    390

Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro  
25                        395                    400                    405

5

10  
15  
20

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val  
410 415 420  
Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys  
425 430 435  
Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val  
440 445 450  
Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg  
455 460 465  
Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro  
470 475 480  
Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro  
485 490 495  
Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val  
500 505 510  
Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr  
515 520 525  
Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu  
530 535 540  
Ile Gly Arg Lys Lys Thr Ser  
545

20

SEQ. ID No. 14

LENGTH: 826

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala Ala Ser Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp  
5 5 10 15  
Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr  
20 25 30  
Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val  
35 40 45  
Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr  
50 55 60  
Asn Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val  
65 70 75  
Tyr Glu Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr  
80 85 90  
Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala  
95 100 105  
Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr  
110 115 120  
20 Gly Tyr Arg Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro  
125 130 135  
Arg Glu Asp Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr  
140 145 150  
Asn Leu Thr Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu  
25 155 160 165

Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr  
170 175 180  
Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro  
185 190 195  
5 Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg  
200 205 210  
Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val  
215 220 225  
Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser  
10 230 235 240  
Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val  
245 250 255  
Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile  
260 265 270  
15 Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Thr Ser Ala Ile Pro  
275 280 285  
Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu  
290 295 300  
Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg  
20 305 310 315  
Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile  
320 325 330  
Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met  
335 340 345  
25 Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr

350                    355                    360

Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn  
365                    370                    375

Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr  
5                        380                    385                    390

Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly  
395                    400                    405

Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln  
410                    415                    420

Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu  
425                    430                    435

Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp  
440                    445                    450

Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile  
455                    460                    465

Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser  
470                    475                    480

Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr  
485                    490                    495

Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val  
20                      500                    505                    510

Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu  
515                    520                    525

Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn  
25                      530                    535                    540

Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Ser Ala  
545 550 555  
Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr  
560 565 570  
5 Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly  
575 580 585  
Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys  
590 595 600  
Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly  
605 610 615  
Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys  
620 625 630  
Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu  
635 640 645  
Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr  
650 655 660  
Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile  
665 670 675  
Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro  
20 680 685 690  
Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr  
695 700 705  
Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu  
710 715 720  
25 Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr

725                    730                    735  
Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro  
740                    745                    750  
Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr  
5                      755                    760                    765  
Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu  
770                    775                    780  
Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr  
785                    790                    795  
Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu  
800                    805                    810  
Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr  
815                    820                    825  
Ser

15                    SEQ. ID No. 15

LENGTH: 38

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

20                    MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCGCT ATTCCTGCAC CAACTGAC

38

SEQ. ID No. 16

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAGGATCCC TAACTAGTCT TTTTCCTTCC AATCAG

36

SEQ. ID No. 17

LENGTH: 1644

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an  
artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60  
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120  
ACCCCCAAGG AGAACGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180  
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240  
20 GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGGCCA 300  
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAAC 360  
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTT CAGCCAATGG CCAGACTCCA 420  
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480  
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540

ATCGACGCCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTCCTGGC CACCACACCC 600  
AATTCCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660  
TATGAGAAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCCA TGTTGTCACA 720  
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780  
5 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCCTGCA 840  
CCAACTGACC TGAAGTTCAC TCAGGTACACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900  
CCCAATGTTG AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960  
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020  
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080  
CAGGGTGTG TCACCACTCT GGAGAACATGTC AGCCCCACCAA GAAGGGCTCG TGTGACAGAT 1140  
GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200  
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260  
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCAGTG ACTACAAGAT CTACCTGTAC 1320  
ACCTTGAATG ACAATGCTCG GAGCTCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380  
15 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440  
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAACCTGG GTCTCCCTCCC 1500  
AGAGAACGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560  
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620  
CTGATTGGAA GGAAAAAGAC TAGT 1644  
20 SEQ. ID No. 18  
LENGTH: 37  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
25 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCCCC ACTGACCTGC GATTCAC

37

SEQ. ID No. 19

LENGTH: 38

5 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAAGATCTC TAACTAGTGG ATGGTTTGTC AATTCTG

38

SEQ. ID No. 20

LENGTH: 2481

TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptyide)

SEQUENCE:

ATGGCAGCTA GCCCCACTGA CCTGCGATTC ACCAACATTG GTCCAGACAC CATGCGTGT 60

20 ACCTGGGCTC CACCCCCATC CATTGATTCA ACCAACTTCC TGGTGCCTTA CTCACCTGTG 120

AAAAATGAGG AAGATGTTGC AGAGTTGTCA ATTCTCCTT CAGACAATGC AGTGGTCTTA 180

ACAAATCTCC TGCCCTGGTAC AGAATATGTA GTGAGTGTCT CCAGTGTCTA CGAACACAT 240

GAGAGCACAC CTCTTAGAGG AAGACAGAAA ACAGGTCTTG ATTCCCCAAC TGGCATTGAC 300

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TTTTCTGATA TTACTGCCAA CTCTTTACT GTGCACTGGA TTGCTCCTCG AGCCACCATC 360  
ACTGGCTACA GGATCCGCCA TCATCCCGAG CACTTCAGTG GGAGACCTCG AGAAGATCGG 420  
GTGCCCACT CTCGGAATT CATCACCCCTC ACCAACCTCA CTCCAGGCAC AGAGTATGTG 480  
GTCAGCATCG TTGCTCTTAA TGGCAGAGAG GAAAGTCCCT TATTGATTGG CCAACAATCA 540  
5 ACAGTTCTG ATGTTCCGAG GGACCTGGAA GTTGTGCTG CGACCCCCAC CAGCCTACTG 600  
ATCAGCTGGG ATGCTCCTGC TGTCACAGTG AGATATTACA GGATCACTTA CGGAGAAACA 660  
GGAGGAAATA GCCCTGTCCA GGAGTTCACT GTGCCTGGGA GCAAGTCTAC AGCTACCATC 720  
AGCGGCCCTTA AACCTGGAGT TGATTATAACC ATCACTGTGT ATGCTGTCAC TGGCCGTGGA 780  
GACAGCCCCG CAAGCAGCAA GCCAATTTC ATTAAATTACC GAACAGAAAT TGACAAACCA 840  
TCCACTAGCG CTATTCTGC ACCAACTGAC CTGAAGTTCA CTCAGGTACAC ACCCACAAAGC 900  
CTGAGCGCCC AGTGGACACC ACCCAATGTT CAGCTCACTG GATATCGAGT GCGGGTGACC 960  
CCCAAGGAGA AGACCGGACC AATGAAAGAA ATCAACCTTG CTCCTGACAG CTCATCCGTG 1020  
GTTGTATCAG GACTTATGGT GGCCACCAAA TATGAAGTGA GTGTCTATGC TCTTAAGGAC 1080  
ACTTTGACAA GCAGACCAGC TCAGGGTGT GTCACCACTC TGGAGAATGT CAGCCCACCA 1140  
AGAAGGGCTC GTGTGACAGA TGCTACTGAG ACCACCATCA CCATTAGCTG GAGAACCAAG 1200  
ACTGAGACGA TCACTGGCTT CCAAGTTGAT GCCGTTCCAG CCAATGGCCA GACTCCAATC 1260  
CAGAGAACCA TCAAGCCAGA TGTCAAGAGC TACACCATCA CAGGTTTACA ACCAGGCAC 1320  
GACTACAAGA TCTACCTGTA CACCTTGAAT GACAATGCTC GGAGCTCCCC TGTGGTCATC 1380  
GACGCCCTCCA CTGCCATTGA TGCACCATCC AACCTGCGTT TCCCTGGCCAC CACACCAAT 1440  
20 TCCTTGCTGG TATCATGGCA GCCGCCACGT GCCAGGATTA CCGGCTACAT CATCAAGTAT 1500  
GAGAAGCCTG GGTCTCCTCC CAGAGAAGTG GTCCCTCGGC CCCGCCCTGG TGTCACAGAG 1560  
GCTACTATTA CTGGCCTGGA ACCGGGAACC GAATATACAA TTTATGTCAT TGCCCTGAAG 1620  
AATAATCAGA AGAGCGAGCC CCTGATTGGA AGGAAAAAGA CTAGCGCTAT TCCTGCACCA 1680  
ACTGACCTGA AGTTCACTCA GGTACACACCC ACAAGCCTGA GCGCCAGTG GACACCACCC 1740  
25 AATGTTCAGC TCACTGGATA TCGAGTGCAG GTGACCCCCA AGGAGAAGAC CGGACCAATG 1800

AAAGAAATCA ACCTTGCTCC TGACAGCTCA TCCGTGGTTG TATCAGGACT TATGGTGGCC 1960  
ACCAAATATG AAGTGAGTGT CTATGCTCTT AAGGACACTT TGACAAGCAG ACCAGCTCAG 1920  
GGTGTGTC CA CACTCTGGA GAATGTCAGC CCACCAAGAA GGGCTCGTGT GACAGATGCT 1980  
ACTGAGACCA CCATCACCAT TAGCTGGAGA ACCAAGACTG AGACGATCAC TGGCTTCCAA 2040  
5 GTTGATGCCG TTCCAGCCAA TGGCCAGACT CCAATCCAGA GAACCATCAA GCCAGATGTC 2100  
AGAACGCTACA CCATCACAGG TTTACAACCA GGCAGTACT ACAAGATCTA CCTGTACACC 2160  
TTGAATGACA ATGCTCGGAG CTCCCCCTGTG GTCATCGACG CCTCCACTGC CATTGATGCA 2220  
CCATCCAACC TCGGTTCCCT GGCCACCACA CCCAATTCCCT TGCTGGTATC ATGGCAGCCG 2280  
CCACGTGCCA GGATTACCGG CTACATCATC AAGTATGAGA AGCCTGGGTC TCCTCCCAGA 2340  
GAAGTGGTCC CTCGGCCCCG CCCTGGTGT ACAGAGGCTA CTATTACTGG CCTGGAACCG 2400  
GGAACCGAAT ATACAATTAA TGTCATTGCC CTGAAGAATA ATCAGAAGAG CGAGCCCCCTG 2460  
ATTGGAAGGA AAAAGACTAG T 2481

SEQ. ID No. 21

LENGTH: 472

15 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

	35	40	45
	Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu		
	50	55	60
	Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln		
5	65	70	75
	His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp		
	80	85	90
	Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe		
	95	100	105
10	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
	125	130	135
15	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
20	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
25	215	220	225

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys  
230 235 240

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg  
245 250 255

5 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
260 265 270

Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp  
275 280 285

Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp  
290 295 300

Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr  
305 310 315

Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro  
320 325 330

Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys  
335 340 345

Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg  
350 355 360

Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro  
20 365 370 375

Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile  
380 385 390

Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp  
395 400 405

25 Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys

410                    415                    420  
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr  
                        425                    430                    435  
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser  
5                        440                    445                    450  
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser  
                      455                        460                    465  
Asn Leu Arg Phe Leu Ala Thr  
                      470

10                    SEQ. ID No. 22

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

15                    MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1                        5                        10                        15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20                        20                        25                        30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
                      35                        40                        45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
                      50                        55                        60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
5 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
95 100 105  
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
110 115 120  
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
125 130 135  
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
140 145 150  
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg  
155 160 165  
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
170 175 180  
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
185 190 195  
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
20 200 205 210  
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
215 220 225  
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys  
230 235 240  
25 Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg

	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Asn Val Ser Pro Pro Arg Arg		
5	275	280	285
	Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp		
	290	295	300
	Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val		
	305	310	315
10	Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp		
	320	325	330
	Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr		
	335	340	345
	Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro		
15	350	355	360
	Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu		
	365	370	375
	Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln		
	380	385	390
20	Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys		
	395	400	405
	Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly		
	410	415	420
	Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr		
25	425	430	435

Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro  
440 445 450  
Leu Ile Gly Arg Lys Lys Thr  
455

5 SEQ. ID No. 23

LENGTH: 549

10 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

15 20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
5	125	130	135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
10	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
15	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
20	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp		
25	275	280	285

Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp  
290 295 300  
Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr  
305 310 315  
5 Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro  
320 325 330  
Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys  
335 340 345  
Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg  
350 355 360  
Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro  
365 370 375  
Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile  
380 385 390  
10 Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp  
395 400 405  
Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys  
410 415 420  
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr  
20 425 430 435  
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser  
440 445 450  
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser  
455 460 465  
25 Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser



Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
5 His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
95 100 105  
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
110 115 120  
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
125 130 135  
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
140 145 150  
155 160 165  
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg  
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
170 175 180  
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
20 185 190 195  
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
200 205 210  
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
215 220 225  
25 Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys

230                    235                    240

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg  
245                    250                    255

Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
5                    260                    265                    270

Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp  
275                    280                    285

Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp  
290                    295                    300

10                    Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr  
305                    310                    315

Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro  
320                    325                    330

Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys  
15                    335                    340                    345

Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg  
350                    355                    360

Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro  
365                    370                    375

20                    Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile  
380                    385                    390

Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp  
395                    400                    405

Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys  
25                    410                    415                    420

Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr  
425 430 435  
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser  
440 445 450  
5 Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser  
455 460 465  
Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser  
470 475 480  
Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr  
485 490 495  
Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg  
500 505 510  
Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr  
515 520 525  
515 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser  
530 535 540  
Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu  
545 550 555  
Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp  
20 560 565 570  
Val Pro Ser Thr

SEQ. ID No. 25

LENGTH: 274

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
95 100 105  
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
110 115 120  
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
125 130 135  
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
140 145 150  
25 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

155                    160                    165  
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
170                    175                    180  
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
5                        185                    190                    195  
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
200                    205                    210  
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
215                    220                    225  
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys  
230                    235                    240  
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg  
245                    250                    255  
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
260                    265                    270  
Thr Glu Ile Asp

SEQ. ID No. 26

LENGTH: 1374

TYPE: nucleic acid

20 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGCCCACTG ACCTGCGATT CACCAACATT GGTCCAGACA CCATGCGTGT CACCTGGCT 60  
CCACCCCCAT CCATTGATTT AACCAAACCTTC CTGGTGCCTT ACTCACCTGT GAAAAATGAG 120  
GAAGATGTTG CAGAGTTGTC AATTTCTCCT TCAGACAATG CAGTGGCTT AACAAATCTC 180  
CTGCCTGGTA CAGAATATGT AGTGAGTGTC TCCAGTGTCT ACGAACAAACA TGAGAGCACA 240  
5 CCTCTTAGAG GAAGACAGAA AACAGGTCTT GATTCCCCAA CTGGCATTGA CTTTCTGAT 300  
ATTACTGCCA ACTCTTTAC TGTGCACTGG ATTGCTCCTC GAGCCACCCT CACTGGCTAC 360  
AGGATCCGCC ATCATCCGA GCACTTCACT GGGAGACCTC GAGAAGATCG GGTGCCAAC 420  
TCTCGGAATT CCATCACCCCT CACCAACCTC ACTCCAGGCA CAGAGTATGT GGTCAGCATE 480  
GTTGCTCTTA ATGGCAGAGA GGAAAGTCCC TTATTGATTG GCCAACAAATC AACAGTTCT 540  
GATGTTCCGA GGGACCTGGA AGTTGTTGCT GCGACCCCCA CCAGCCTACT GATCAGCTGG 600  
GATGCTCCTG CTGTCACAGT GAGATATTAC AGGATCACTT ACGGAGAAC AGGAGGAAAT 660  
AGCCCTGTCC AGGAGTCAC TGTGCCTGGG AGCAAGTCTA CAGCTACCAT CAGCGGCCTT 720  
AAACCTGGAG TTGATTATAC CATCACTGTG TATGCTGTCA CTGGCCGTGG AGACAGCCCC 780  
GCAAGCAGCA AGCCAATTTC CATTAATTAC CGAACAGAAA TTGACAAACC ATCCATGGCA 840  
GCCGGGAGCA TCACCACGCT GCCCGCCTTG CCCGAGGATG GCGGCAGCGG CGCCTTCCCG 900  
CCCGGCCACT TCAAGGACCC CAAGCGGCTG TACTGCAAAA ACGGGGGCTT CTTCCTGCGC 960  
ATCCACCCCG ACGGCCGAGT TGACGGGGTC CGGGAGAAGA GCGACCCCTCA CATCAAGCTA 1020  
CAACTTCAAG CAGAAGAGAG AGGAGTTGTG TCTATCAAAG GAGTGTGTGC TAACCGTTAC 1080  
CTGGCTATGA AGGAAGATGG AAGATTACTG GCTTCTAAAT GTGTTACGGA TGAGTGTTC 1140  
20 TTTTTGAAC GATTGGAATC TAATAACTAC AATACTTACC GCTCAAGGAA ATACACCAGT 1200  
TGGTATGTGG CACTGAAACG AACTGGCAG TATAAACTTG GATCCAAAAC AGGACCTGGG 1260  
CAGAAAGCTA TACTTTTCT TCCAATGTCT GCTGCTAGCG ACGAGCTTCC CCAACTGGTA 1320  
ACCCCTCCAC ACCCAATCT TCATGGACCA GAGATCTTGG ATGTTCCCTTC CACA 1374

LENGTH: 1416

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

CCCCACTGACC TCGGATTACAC CAACATTGGT CCAGACACCA TGCCTGTAC CTGGGCTCCA 60  
CCCCCATCCA TTGATTTAAC CAACTTCCTG GTGCGTTACT CACCTGTGAA AAATGAGGAA 120  
GATGTTGCAG AGTTGTCAAT TTCTCCTTCA GACAATGCAG TGGTCTTAAC AAATCTCCTG 180  
CCTGGTACAG AATATGTAGT GAGTGTCTCC AGTGTCTACG AACAAACATGA GAGCACACCT 240  
CTTAGAGGAA GACAGAAAAC AGGTCTTGAT TCCCCAACTG GCATTGACTT TTCTGATATT 300  
ACTGCCAACT CTTTACTGT GCACTGGATT GCTCCTCGAG CCACCATCAC TGGCTACAGG 360  
ATCCGCCATC ATCCCGAGCA CTTCAGTGGG AGACCTCGAG AAGATCGGGT GCCCCACTCT 420  
CGGAATTCCA TCACCCCTCAC CAAACCTCACT CCAGGCACAG AGTATGTGGT CAGCATCGTT 480  
GCTCTTAATG GCAGAGAGGA AAGTCCCTTA TTGATTGGCC ACAAATCAAC AGTTTCTGAT 540  
GTTCCGAGGG ACCTGGAAGT TGTTGCTGCG ACCCCCACCA GCCTACTGAT CAGCTGGGAT 600  
GCTCCTGCTG TCACAGTGAG ATATTACAGG ATCACTTACG GAGAAACAGG AGGAAATAGC 660  
CCTGTCCAGG AGTTCACTGT GCCTGGGAGC AAGTCTACAG CTACCATCAG CGGCCTTAAA 720  
20 CCTGGAGTTG ATTATAACCAT CACTGTGTAT GCTGTCACTG GCCGTGGAGA CAGCCCCGCA 780  
AGCAGCAAGC CAATTCCAT TAATTACCGA ACAGAAATTG ACAAAACCATC CATGGCTATT 840  
CCTGCACCAA CTGACCTGAA GTTCACTCAG GTCACACCCA CAAGCCTGAG CGCCCAGTGG 900  
ACACCCACCA ATGTTCAGCT CACTGGATAT CGAGTGCAGG TGACCCCCAA GGAGAAAGACC 960  
GGACCAATGA AAGAAATCAA CCTTGCTCCT GACAGCTCAT CCGTGGTTGT ATCAGGACTT 020  
25 ATGGTGGCCA CCAAATATGA AGTGAGTGTC TATGCTCTTA AGGACACTTT GACAAGCAGA 1080

CCAGCTCAGG GTGTTGTCAC CACTCTGGAG AATGTCAGCC CACCAAGAAG GGCTCGTGTG 1140  
ACAGATGCTA CTGAGACCAAC CATCACCAATT AGCTGGAGAA CCAAGACTGA GACGATCACT 1200  
GGCTTCCAAG TTGATGCCGT TCCAGCCAAT GGCCAGACTC CAATCCAGAG AACCATCAAG 1260  
CCAGATGTCA GAAGCTACAC CATCACAGGT TTACAACCAG GCACTGACTA CAAGATCTAC 1320  
5 CTGTACACCT TGAATGACAA TGCTCGGAGC TCCCCTGTGG TCATCGACGC CTCCACTGCC 1380  
ATTGATGCAC CATCCAACCT GCGTTTCCTG GCCACC 1416

SEQ. ID No. 28

LENGTH: 35

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg

15 1 5 10 15

Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr

20 20 25 30

Gly Lys Pro Gly Pro

35

20 SEQ. ID No. 29

LENGTH: 302

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

5 1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

95 100 105

Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg

110 115 120

20 Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp

125 130 135

Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr

140 145 150

Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

25 155 160 165

Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
170 175 180

Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
185 190 195

5 Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
200 205 210

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
215 220 225

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys  
230 235 240

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg  
245 250 255

Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg  
260 265 270

Thr Glu Ile Asp Lys Pro Ser Asp Glu Leu Pro Gln Leu Val Thr  
275 280 285

Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro  
290 295 300

Ser Thr

20 SEQ. ID No. 30

LENGTH: 573

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ala Ala Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr

5 5 10 15

5 Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn  
20 25 30

Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys  
35 40 45

Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser  
50 55 60

Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser  
65 70 75

Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly  
80 85 90

Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg  
95 100 105

Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr  
110 115 120

Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala  
20 125 130 135

Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg  
140 145 150

Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile  
155 160 165

25 Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val

170                    175                    180

Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe  
185                    190                    195

Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro  
5                    200                    205                    210

Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly  
215                    220                    225

Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr  
230                    235                    240

Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile  
245                    250                    255

Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile  
260                    265                    270

Gly Arg Lys Lys Thr Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe  
275                    280                    285

Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro  
290                    295                    300

Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu  
305                    310                    315

20                    Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser  
320                    325                    330

Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val  
335                    340                    345

Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln  
25                    350                    355                    360

Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala  
365 370 375

Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg  
380 385 390

5 Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro  
395 400 405

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val  
410 415 420

Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys  
425 430 435

Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val  
440 445 450

Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg  
455 460 465

15 Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro  
470 475 480

Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro  
485 490 495

Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val  
20 500 505 510

Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr  
515 520 525

Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu  
530 535 540

25 Ile Gly Arg Lys Lys Thr Ser Asp Glu Leu Pro Gln Leu Val Thr

545                    550                    555  
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro  
560                    565                    570  
Ser Thr Ser

5       SEQ. ID No. 31

LENGTH: 37

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

10      MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCAAT GTCAGCCCCAC CAAGAAG                    37

SEQ. ID No. 32

LENGTH: 37

15      TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

20      AAAGGATCCC TAACTAGTGG AAGGAACATC CAAGATC                    37

SEQ. ID No. 33

LENGTH: 1722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial  
5 polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60  
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCAGGGTG 120  
ACCCCCAAGG AGAACGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180  
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240  
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCCA CTCTGGAGAA TGTCAGCCC 300  
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAAC 360  
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTT CAGCCAATGG CCAGACTCCA 420  
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480  
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540  
ATCGACGCCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTCCCTGGC CACCACACCC 600  
AATTCCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660  
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCC CTTGTGTACA 720  
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780  
20 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCCTGCA 840  
CCAACTGACC TGAAGTTCAC TCAGGTACCA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900  
CCCAATGTTG AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960  
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020  
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080  
25 CAGGGTGTG TCACCACTCT GGAGAATGTC AGCCCCACCA GAAGGGCTCG TGTGACAGAT 1140

GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200  
CAAGTTGATG CCGTTCAGC CAATGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260  
GTCAGAAGCT ACACCATCAC AGGTTACAA CCAGGCCTG ACTACAAGAT CTACCTGTAC 1320  
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380  
5 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440  
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAACGCTGG GTCTCCTCCC 1500  
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560  
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620  
CTGATTGGAA GGAAAAGAC TAGCGACGAG CTTCCCCAAC TGGTAACCCT TCCACACCCCC 1680  
AATCTTCATG GACCAGAGAT CTTGGATGTT CCTTCCACTA GT 1722

SEQ. ID No. 34

LENGTH: 412

TYPE: amino acid

STRANDEDNESS: single

15 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln			
	5	10	15
20 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu	20	25	30
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys	35	40	45
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp			

50                        55                        60  
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
65                        70                        75  
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
5                        80                        85                        90  
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
95                        100                        105  
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
110                        115                        120  
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp  
125                        130                        135  
Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His  
140                        145                        150  
Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met  
155                        160                        165  
Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys  
170                        175                        180  
Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser  
185                        190                        195  
20                        Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe  
200                        205                        210  
Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly Arg  
215                        220                        225  
Gly Ile Pro Arg Asn Ser Gly Ala Pro Pro Arg Leu Ile Cys Asp  
25                        230                        235                        240

Ser Arg Val Leu Gln Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu  
245 250 255  
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn  
260 265 270  
5 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
275 280 285  
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala  
290 295 300  
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn  
305 310 315  
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala  
320 325 330  
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly  
335 340 345  
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
350 355 360  
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg  
365 370 375  
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly  
20 380 385 390  
Glu Ala Cys Arg Thr Gly Asp Arg Leu Ala Met Asp Pro Leu Glu  
395 400 405  
Ser Thr Arg Ala Ala Ala Ser  
410

SEQ. ID No. 35

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GCTCCCTCTG GGCCTCCCAG TCCT

24

SEQ. ID No. 36

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

15 SEQUENCE:

GTTGGTGAGG GAGGTGGTGG ATAT

24

SEQ. ID No. 37

LENGTH: 33

TYPE: nucleic acid

20 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GGCCTCCCGA ATTCCGGTGC CCCACCACGC CTC

33

SEQ. ID No. 38

LENGTH: 33

TYPE: nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCCACGTGGA TCCATGGCTA ATCTGTCCCC TGT

33

10 SEQ. ID No. 39

LENGTH: 1239

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGTCCCCTA TACTAGGTTA TTGGAAAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60

TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTGTATG AGCGCGATGA AGGTGATAAA 120

20 TGGCGAAACA AAAAGTTGA ATTGGGTTTG GAGTTCCCA ATCTTCCTTA TTATATTGAT 180

GGTGATGTTA AATTAACACA GTCTATGCC ATCATACGTT ATATAGCTGA CAAGCACAAAC 240

ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTCAA TGCTTGAAGG AGCGGTTTG 300

GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

	GATTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTCG AAGATCGTT ATGTCATAAA	420
	ACATATTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT	480
	GTTGTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTTAAA	540
	AAACGTATTG AAGCTATCCC ACAAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA	600
5	TGGCCTTGCA AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT	660
	CTGATCGAAG GTCGTGGAT CCCCAGGAAT TCCGGTGCCTC CACCACGCCCT CATCTGTGAC	720
	AGCCGAGTCC TGCAGAGGTA CCTCTTGGAG GCCAAGGGAGG CCGAGAATAT CACGACGGGC	780
	TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTC	840
	TATGCCTGGA AGAGGATGGA GGTCGGGCAG CAGGCCGTAG AAGTCTGGCA GGGCCTGGCC	900
10	CTGCTGTCGG AAGCTGTCCT GCGGGGCCAG GCCCTGTTGG TCAACTCTTC CCAGCCGTGG	960
	GAGCCCCCTGC AGCTGCATGT GGATAAAGCC GTCAGTGGCC TTCGCAGCCT CACCACTCTG	1020
	CTTCGGGCTC TGGGAGGCCA GAAGGAAGCC ATCTCCCCTC CAGATGCCGC CTCAGCTGCT	1080
	CCACTCCGAA CAATCACTGC TGACACTTTC CGCAAACCTCT TCCGAGTCTA CTCCAATTTC	1140
	CTCCGGGAA AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATTAGCC	1200
15	ATGGATCCTC TAGAGTCGAC TCGAGCGGCC GCATCGTGA	1239